



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: WILLIAMS, Lewis T.
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(ii) TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS

(iii) NUMBER OF SEQUENCES: 14

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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/461,917
(B) FILING DATE: 05-JUN-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/309,322
(B) FILING DATE: 10-FEB-1989

(viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/151,414
(B) FILING DATE: 02-FEB-1988

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(C) REFERENCE/DOCKET NUMBER: 2307K-267-2-4

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 129..3398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGAGCTAC	AGGGAGAGAA	ACAGAGGAGG	AGACTGCAAG	AGATCATTGG	AGGCCGTGGG	60									
CACGCTCTTT	ACTCCATGTG	TGGGACATTC	ATTGCGGAAT	AACATCGGAG	GAGAAGTTTC	120									
CCAGAGCT	ATG GGG ACT TCC	CAT CCG GCG	TTC CTG GTC	TTA GGC TGT	CTT	170									
Met	Gly	Thr	Ser	His	Pro	Ala	Phe	Leu	Val	Leu	Gly	Cys	Leu		
1							5					10			
CTC ACA GGG CTG AGC CTA ATC CTC TGC CAG CTT TCA TTA CCC TCT ATC													218		
Leu	Thr	Gly	Leu	Ser	Leu	Ile	Leu	Cys	Gln	Leu	Ser	Leu	Pro	Ser	Ile
15							20			25			30		
CTT CCA AAT GAA AAT GAA AAG GTT GTG CAG CTG AAT TCA TCC TTT TCT													266		
Leu	Pro	Asn	Glu	Asn	Glu	Lys	Val	Val	Gln	Leu	Asn	Ser	Ser	Phe	Ser
35							40						45		
CTG AGA TGC TTT GGG GAG AGT GAA GTG AGC TGG CAG TAC CCC ATG TCT													314		
Leu	Arg	Cys	Phe	Gly	Glu	Ser	Glu	Val	Ser	Trp	Gln	Tyr	Pro	Met	Ser
50							55						60		
GAA GAA GAG AGC TCC GAT GTG GAA ATC AGA AAT GAA GAA AAC AAC AGC													362		
Glu	Glu	Glu	Ser	Ser	Asp	Val	Glu	Ile	Arg	Asn	Glu	Glu	Asn	Asn	Ser
65							70						75		
GGC CTT TTT GTG ACG GTC TTG GAA GTG AGC AGT GCC TCG GCG GCC CAC													410		
Gly	Leu	Phe	Val	Thr	Val	Leu	Glu	Val	Ser	Ser	Ala	Ser	Ala	Ala	His
80							85						90		
ACA GGG TTG TAC ACT TGC TAT TAC AAC CAC ACT CAG ACA GAA GAG AAT													458		
Thr	Gly	Leu	Tyr	Thr	Cys	Tyr	Tyr	Asn	His	Thr	Gln	Thr	Glu	Glu	Asn
95							100						105		110
GAG CTT GAA GGC AGG CAC ATT TAC ATC TAT GTG CCA GAC CCA GAT GTA													506		
Glu	Leu	Glu	Gly	Arg	His	Ile	Tyr	Ile	Tyr	Val	Pro	Asp	Pro	Asp	Val
115							120						125		
GCC TTT GTA CCT CTA GGA ATG ACG GAT TAT TTA GTC ATC GTG GAG GAT													554		
Ala	Phe	Val	Pro	Leu	Gly	Met	Thr	Asp	Tyr	Leu	Val	Ile	Val	Glu	Asp
130							135						140		
GAT GAT TCT GCC ATT ATA CCT TGT CGC ACA ACT GAT CCC GAG ACT CCT													602		
Asp	Asp	Ser	Ala	Ile	Ile	Pro	Cys	Arg	Thr	Thr	Asp	Pro	Glu	Thr	Pro
145							150						155		
GTA ACC TTA CAC AAC AGT GAG GGG GTG GTA CCT GCC TCC TAC GAC AGC													650		
Val	Thr	Leu	His	Asn	Ser	Glu	Gly	Val	Val	Pro	Ala	Ser	Tyr	Asp	Ser
160							165						170		
AGA CAG GGC TTT AAT GGG ACC TTC ACT GTA GGG CCC TAT ATC TGT GAG													698		
Arg	Gln	Gly	Phe	Asn	Gly	Thr	Phe	Thr	Val	Gly	Pro	Tyr	Ile	Cys	Glu
175							180						185		190
GCC ACC GTC AAA GGA AAG AAG TTC CAG ACC ATC CCA TTT AAT GTT TAT													746		
Ala	Thr	Val	Lys	Gly	Lys	Phe	Gln	Thr	Ile	Pro	Phe	Asn	Val	Tyr	
195							200						205		
GCT TTA AAA GCA ACA TCA GAG CTG GAT CTA GAA ATG GAA GCT CTT AAA													794		
Ala	Leu	Lys	Ala	Thr	Ser	Glu	Leu	Asp	Leu	Glu	Met	Glu	Ala	Leu	Lys
210							215						220		
ACC GTG TAT AAG TCA GGG GAA ACG ATT GTG GTC ACC TGT GCT GTT TTT													842		
Thr	Val	Tyr	Lys	Ser	Gly	Glu	Thr	Ile	Val	Val	Thr	Cys	Ala	Val	Phe
225							230						235		
AAC AAT GAG GTG GTT GAC CTT CAA TGG ACT TAC CCT GGA GAA GTG AAA													890		
Asn	Asn	Glu	Val	Val	Asp	Leu	Gln	Trp	Thr	Tyr	Pro	Gly	Glu	Val	Lys
240							245						250		

GGC AAA GGC ATC ACA ATG CTG GAA GAA ATC AAA GTC CCA TCC ATC AAA Gly Lys Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys 255 260 265 270	938
TTG CTG TAC ACT TTG ACG GTC CCC GAG GCC ACG GTG AAA GAC AGT CGA Leu Val Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly 275 280 285	986
GAT TAC GAA TGT GCT GCC CGC CAG GCT ACC AGG GAG GTC AAA GAA ATG Asp Tyr Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met 290 295 300	1034
AAG AAA GTC ACT ATT TCT GTC CAT GAG AAA GGT TTC ATT GAA ATC AAA Lys Lys Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys 305 310 315	1082
CCC ACC TTC AGC CAG TTG GAA GCT GTC AAC CTG CAT GAA GTC AAA CAT Pro Thr Phe Ser Gln Leu Ala Val Asn Leu His Glu Val Lys His 320 325 330	1130
TTT GTT GTA GAG GTG CGG GCC TAC CCA CCT CCC AGG ATA TCC TGG CTG Phe Val Val Glu Val Arg Ala Tyr Pro Pro Arg Ile Ser Trp Leu 335 340 345 350	1178
AAA AAC AAT CTG ACT CTG ATT GAA AAT CTC ACT GAG ATC ACC ACT GAT Lys Asn Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp 355 360 365	1226
GTG GAA AAG ATT CAG GAA ATA AGG TAT CGA AGC AAA TTA AAG CTG ATC Val Glu Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile 370 375 380	1274
CGT GCT AAG GAA GAA GAC AGT GGC CAT TAT ACT ATT GTA GCT CAA AAT Arg Ala Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn 385 390 395	1322
GAA GAT GCT GTG AAG AGC TAT ACT TTT GAA CTG TTA ACT CAA GTT CCT Glu Asp Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro 400 405 410	1370
TCA TCC ATT CTG GAC TTG GTC GAT GAT CAC CAT GGC TCA ACT GGG GGA Ser Ser Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly 415 420 425 430	1418
CAG ACG GTG AGG TGC ACA GCT GAA GGC ACG CCG CTT CCT GAT ATT GAG Gln Thr Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu 435 440 445	1466
TGG ATG ATA TGC AAA GAT ATT AAG AAA TGT AAT AAT GAA ACT TCC TGG Trp Met Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp 450 455 460	1514
ACT ATT TTG GCC AAC AAT GTC TCA AAC ATC ATC ACG GAG ATC CAC TCC Thr Ile Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser 465 470 475	1562
CGA GAC AGG AGT ACC GTG GAG GGC CGT GTG ACT TTC GCC AAA GTG GAG Arg Asp Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu 480 485 490	1610
GAG ACC ATC GCC GTG CGA TGC CTG GCT AAG AAT CTC CTT GGA GCT GAG Glu Thr Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu 495 500 505 510	1658
AAC CGA GAG CTG AAG CTG GTG GCT CCC ACC CTG CGT TCT GAA CTC ACG Asn Arg Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr 515 520 525	1706

GTG GCT GCT GCA GTC CTG GTG CTG TTG GTG ATT GTG ATC ATC TCA CTT Val Ala Ala Ala Val Leu Val Leu Val Ile Val Ile Ile Ser Leu 530 535 540	1754
ATT GTC CTG GTT GTC ATT TGG AAA CAG AAA CCG AGG TAT GAA ATT CGC Ile Val Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg 545 550 555	1802
TGG AGG GTC ATT GAA TCA ATC AGC CCA GAT GGA CAT GAA TAT ATT TAT Trp Arg Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr 560 565 570	1850
GTG GAC CCG ATG CAG CTG CCT TAT GAC TCA AGA TGG GAG TTT CCA AGA Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg 575 580 585 590	1898
GAT GGA CTA GTG CTT GGT CGG GTC TTG GGG TCT GGA GCG TTT GGG AAG Asp Gly Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys 595 600 605	1946
GTG GTT GAA GGA ACA GCC TAT GGA TTA AGC CGG TCC CAA CCT GTC ATG Val Val Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met 610 615 620	1994
AAA GTT GCA GTG AAG ATG CTA AAA CCC ACG GCC AGA TCC AGT GAA AAA Lys Val Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys 625 630 635	2042
CAA GCT CTC ATG TCT GAA CTG AAG ATA ATG ACT CAC CTG GGG CCA CAT Gln Ala Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His 640 645 650	2090
TTG AAC ATT GTA AAC TTG CTG GGA GCC TGC ACC AAG TCA GGC CCC ATT Leu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile 655 660 665 670	2138
TAC ATC ATC ACA GAG TAT TGC TTC TAT GGA GAT TTG GTC AAC TAT TTG Tyr Ile Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu 675 680 685	2186
CAT AAG AAT AGG GAT AGC TTC CTG AGC CAC CAC CCA GAG AAG CCA AAG His Lys Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys 690 695 700	2234
AAA GAG CTG GAT ATC TTT GGA TTG AAC CCT GCT GAT GAA AGC ACA CGG Lys Glu Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg 705 710 715	2282
AGC TAT GTT ATT TTA TCT TTT GAA AAC AAT GGT GAC TAC ATG GAC ATG Ser Tyr Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met 720 725 730	2330
AAG CAG GCT GAT ACT ACA CAG TAT GTC CCC ATG CTA GAA AGG AAA GAG Lys Gln Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu 735 740 745 750	2378
GTT TCT AAA TAT TCC GAC ATC CAG AGA TCA CTC TAT GAT CGT CCA GCC Val Ser Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala 755 760 765	2426
TCA TAT AAG AAG AAA TCT ATG TTA GAC TCA GAA GTC AAA AAC CTC CTT Ser Tyr Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu 770 775 780	2474
TCA GAT GAT AAC TCA GAA GGC CTT ACT TTA TTG GAT TTG TTG AGC TTC Ser Asp Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Phe 785 790 795	2522

ACC TAT CAA GTT GCC CGA GGA ATG GAG TTT TTG GCT TCA AAA AAT TGT	2570
Thr Tyr Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys	
800 805 810	
GTC CAC CGT GAT CTG GCT GCT CGC AAC GTT CTC CTG GCA CAA GGA AAA	2618
Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys	
815 820 825 830	
ATT GTG AAG ATC TGT GAC TTT GGC CTG GCC AGA GAC ATC ATG CAT GAT	2666
Ile Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp	
835 840 845	
TCG AAC TAT GTG TCG AAA GGC AGT ACC TTT CTG CCC GTG AAG TGG ATG	2714
Ser Asn Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met	
850 855 860	
GCT CCT GAG AGC ATC TTT GAC AAC CTC TAC ACC ACA CTG AGT GAT GTC	2762
Ala Pro Glu Ser Ile Phe Asp Asn Leu Tyr Thr Leu Ser Asp Val	
865 870 875	
TGG TCT TAT GGC ATT CTG CTC TGG GAG ATC TTT TCC CTT GGT GGC ACC	2810
Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr	
880 885 890	
CCT TAC CCC GGC ATG ATG GTG GAT TCT ACT TTC TAC AAT AAG ATC AAG	2858
Pro Tyr Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys	
895 900 905 910	
AGT GGG TAC CGG ATG GCC AAG CCT GAC CAC GCT ACC AGT GAA GTC TAC	2906
Ser Gly Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr	
915 920 925	
GAG ATC ATG GTG AAA TGC TGG AAC AGT GAG CCG GAG AAG AGA CCC TCC	2954
Glu Ile Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser	
930 935 940	
TTT TAC CAC CTG AGT GAG ATT GTG GAG AAT CTG CTG CCT GGA CAA TAT	3002
Phe Tyr His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr	
945 950 955	
AAA AAG AGT TAT GAA AAA ATT CAC CTG GAC TTC CTG AAG AGT GAC CAT	3050
Lys Lys Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His	
960 965 970	
CCT GCT GTG GCA CGC ATG CGT GTG GAC TCA GAC AAT GCA TAC ATT GGT	3098
Pro Ala Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly	
975 980 985 990	
GTC ACC TAC AAA AAC GAG GAA GAC AAG CTG AAG GAC TGG GAG GGT GGT	3146
Val Thr Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly	
995 1000 1005	
CTG GAT GAG CAG AGA CTG AGC GCT GAC AGT GGC TAC ATC ATT CCT CTG	3194
Leu Asp Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu	
1010 1015 1020	
CCT GAC ATT GAC CCT GTC CCT GAG GAG GAG GAC CTG GGC AAG AGG AAC	3242
Pro Asp Ile Asp Pro Val Pro Glu Glu Asp Leu Gly Lys Arg Asn	
1025 1030 1035	
AGA CAC AGC TCG CAG ACC TCT GAA GAG AGT GCC ATT GAG ACG GGT TCC	3290
Arg His Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser	
1040 1045 1050	
AGC AGT TCC ACC TTC ATC AAG AGA GAG GAC GAG ACC ATT GAA GAC ATC	3338
Ser Ser Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile	
1055 1060 1065 1070	

GAC ATG ATG GAC GAC ATC GGC ATA GAC TCT TCA GAC CTG GTG GAA GAC Asp Met Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp 1075 1080 1085	3386
AGC TTC CTG TAA CTGGCGGATT CGAGGGGTTTC CTTCCACTTC TGGGGCCACC Ser Phe Leu * 1090	3438
TCTGGATCCC GTTCAGAAAA CCACTTTATT GCAATGCGGA GGTTGAGAGG AGGACTTGTT TGATGTTAA AGAGAAGTTC CCAGCCAAGG GCCTCGGGGA GCCTTCTAA ATATGAATGA ATGGGATATT TTGAAATGAA CTTTGTCACT GTTGCCTCTT GCAATGCCTC AGTAGCATCT CAGTGGTGTG TGAAGTTGG AGATAGATGG ATAAGGGAAT AATAGGCCAC AGAAGGTGAA CTTTCTGCTT CAAGGACATT GGTGAGAGTC CAACAGACAC AATTTATACT GCGACAGAAC TTCAGCATTG TAATTATGTA AATAACTCTA ACCACGGCTG TGTTTAGATT GTATTAAC TCTTCTTGG ACTTCTGAAG AGACCACTCA ATCCATCCAT GTACTCCCT CTTGAAACCT GATGTCAGCT GCTGTTGAAC TTTTTAAAGA AGTGCATGAA AAACCATTAA TGACCTTAA AGGTACTGGT ACTATAGCAT TTTGCTATCT TTTTTAGTGT TAAAGAGATA AAGAATAATA ATTAACCAAC CTTGTTAAT AGATTTGGGT CATTAGAAG CCTGACAAC CATTTCATA TTGTAATCTA TGTTTATAAT ACTACTACTG TTATCAGTAA TGCTAAATGT GTAATAATGT AACATGATT CCCTCCACAC AAAGCACAAT TTAAAAACAA TCCTTACTAA GTAGGTGATG AGTTTGACAG TTTTGACAT TTATATTAAA TAACATGTTT CTCTATAAG TATGGTAATA GCTTTAGTGA ATTAAATTAA GTTGAGCATA GAGAACAAAG TAAAAGTAGT GTTGTCCAGG AAGTCAGAAT TTTTAACTGT ACTGAATAGG TTCCCCAATC CATCGTATTA AAAACAAATT AACTGCCCTC TGAAATAATG GGATTAGAAA CAAACAAAAC TCTTAAGTCC TAAAAGTTCT CAATGTAGAG GCATAAACCT GTGCTGAACA TAACTTCTCA TGTATATTAC CCAATGGAAA ATATAATGAT CAGCGAAAA GACTGGATT GCAGAAGTTT TTTTTTTTT TCTTCTTGCC TGATGAAAGC TTTGGCGACC CCAATATAATG TATTTTTGA ATCTATGAAC CTGAAAAGGG TCACAAAGGA TGCCCAGACA TCAGCCTCCT TCTTCACCC CTTACCCAA AGAGAAAGAG TTTGAAACTC GAGACCATAA AGATATTCTT TAGTGGAGGC TGGAAGTGCA TTAGCCTGAT CCTCAGTTCT CAAATGTGTG TGGCAGCCAG GTAGACTAGT ACCTGGTTT CCATCCTTGA GATTCTGAAG TATGAAGTCT GAGGGAAACC AGAGTCTGTA TTTTTCTAAA CTCCCTGGCT GTTCTGATCG GCCAGGTTTC GGAAACACTG ACTTAGGTTT CAGGAAGTTG CCATGGAAA CAAATAATT GAACTTGGA ACAGGGTTCT TAAGTTGGTG CGTCCTTCGG ATGATAAATT TAGGAACCGA AGTCCAATCA CTGTAAATTA CGGTAGATCG ATCGTTAACG CTGGAATTAA ATTGAAAGGT CAGAATCGAC TCCGACTCTT TCGATTCAA ACCAAAACG TCCAAAAGGT TTTCATTTCT ACGATGAAGG GTGACATACC CCCTCTAACT TGAAAGGGC AGAGGGCAGA AGAGCGGAGG GTGAGGTATG GGGCGGTTCC TTTCCGTACA TGTTTTAAT ACGTTAAC ACAAGGTTCA GAGACACATT GGTGAGTCA CAAAACCACCC TTTTTGTAA AATTCAAAAT	3498 3558 3618 3678 3738 3798 3858 3918 3978 4038 4098 4158 4218 4278 4338 4398 4458 4518 4578 4638 4698 4758 4818 4878 4938 4998 5058 5118 5178 5238

GACTATTAAA	CTCCAATCTA	CCCTCCTACT	TAACAGTGTA	GATAGGTGTG	ACAGTTGTC	5298
CAACCAACACC	CAAGTAACCG	TAAGAAACGT	TATGACGAAT	TAACGACTAT	GGTATACTTA	5358
CTTTGTACCC	GACACTAATG	ACGTTAGTGA	CACGATAGCC	GTCTACTACG	AAACCTTCTA	5418
CGTCTTCGTT	ATTATTCAT	GAACTGATGG	ATGACCACAT	TAGAGTTACG	TTCGGGGTTG	5478
AAAGAATAGG	TTGAAAAAGT	ATCATTACCG	CTTCTGACTC	GGTCTAACCG	GTTAATTTTT	5538
CTTTGGACT	GATCCAAGAC	ATCTCGGTTA	ATCTGAACCT	TATGCAAACA	CAAAGATCTT	5598
AGTGTGAGT	TCGTAAGACA	AATAGCGAGT	GAGAGGAAAC	ATGTCGGAAT	AAAACAACCA	5658
CGAAACGTAA	AACTATAACG	ACACTCGGAA	CGTACTGTAG	TACTCCGGCC	TACTTTGAAG	5718
AGTCAGGTCTG	TCAAAGGTCA	GGATTGTTA	CGAGGGTGG	CTTAAACATA	TACTGACGTA	5778
AACACCCACA	CACACACAAA	AGTCGTTAA	GGTCTAAACA	AAGGAAAACC	GGAGGACGTT	5838
TCAGAGGTCT	TCTTTAAAC	GGTTAGAAAG	GATGAAAGAT	AAAAATACTA	CTGTTAGTTT	5898
CGGCCGGACT	CTTTGTGATA	AACACTGAAA	AATTGCTAA	TCACTACAGG	AATTTTACAC	5958
CAGACGGTTA	GACATGTTT	ACCAGGATAA	AAACACTTCT	CCCTGTATTC	TATTTTACTA	6018
CAATATGTAG	TTATACATAT	ATACATAAAG	ATATATCTGA	ACCTCTTATG	ACGGTTTTGT	6078
AAATACTGTT	CGACATAGTG	ACGGAAGCAA	ATATAAAAAA	ATTGACACTA	TTAGGGGTGT	6138
CCGTGTAATT	GACAACGTGA	AAACTTACAG	GTTTAAATA	AAAATCTTT	ATTATTTTC	6198
TTTCTATGAA	TGTACAAGGG	TTTGTTACC	ACACCACTTA	CACACTCTT	TTGATTGAAC	6258
TATCCCAGAT	GGTTATGTTT	TACATAATGC	TTACGGGGAC	AAGTACAAAAA	ACAAAATTTT	6318
GCACATTTAC	TTCTAGAAAT	ATAAAGTTAT	TTACTATATA	TTAAATTCC	TTAAG	6373

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1090 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Thr	Ser	His	Pro	Ala	Phe	Leu	Val	Leu	Gly	Cys	Leu	Leu	Thr
1					5				10					15	

Gly	Leu	Ser	Leu	Ile	Leu	Cys	Gln	Leu	Ser	Leu	Pro	Ser	Ile	Leu	Pro
				20				25				30			

Asn	Glu	Asn	Glu	Lys	Val	Val	Gln	Leu	Asn	Ser	Ser	Phe	Ser	Leu	Arg
					35		40				45				

Cys	Phe	Gly	Glu	Ser	Glu	Val	Ser	Trp	Gln	Tyr	Pro	Met	Ser	Glu	Glu
	50				55				60						

Glu	Ser	Ser	Asp	Val	Glu	Ile	Arg	Asn	Glu	Glu	Asn	Asn	Ser	Gly	L u
				65		70			75				80		

Phe	Val	Thr	Val	Leu	Glu	Val	Ser	Ser	Ala	Ser	Ala	Ala	His	Thr	Gly
				85			90						95		

Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu
 100 105 110

Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe
 115 120 125

Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp
 130 135 140

Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr
 145 150 155 160

Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln
 165 170 175

Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr
 180 185 190

Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu
 195 200 205

Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val
 210 215 220

Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn
 225 230 235 240

Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys
 245 250 255

Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val
 260 265 270

Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr
 275 280 285

Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys
 290 295 300

Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr
 305 310 315 320

Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val
 325 330 335

Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn
 340 345 350

Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu
 355 360 365

Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala
 370 375 380

Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp
 385 390 395 400

Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser
 405 410 415

Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr
 420 425 430

Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met
 435 440 445

Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile
 450 455 460
 Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp
 465 470 475 480
 Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr
 485 490 495
 Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg
 500 505 510
 Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala
 515 520 525
 Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val
 530 535 540
 Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg
 545 550 555 560
 Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp
 565 570 575
 Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly
 580 585 590
 Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val
 595 600 605
 Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val
 610 615 620
 Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala
 625 630 635 640
 Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn
 645 650 655
 Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile
 660 665 670
 Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys
 675 680 685
 Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu
 690 695 700
 Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr
 705 710 715 720
 Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln
 725 730 735
 Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser
 740 745 750
 Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala Ser Tyr
 755 760 765
 Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu Ser Asp
 770 775 780
 Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Ph Thr Tyr
 785 790 795 800

Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His
 805 810 815
 Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val
 820 825 830
 Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn
 835 840 845
 Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro
 850 855 860
 Glu Ser Ile Phe Asp Asn Leu Tyr Thr Leu Ser Asp Val Trp Ser
 865 870 875 880
 Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr
 885 890 895
 Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly
 900 905 910
 Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile
 915 920 925
 Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr
 930 935 940
 His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys
 945 950 955 960
 Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala
 965 970 975
 Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr
 980 985 990
 Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp
 995 1000 1005
 Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp
 1010 1015 1020
 Ile Asp Pro Val Pro Glu Glu Asp Leu Gly Lys Arg Asn Arg His
 1025 1030 1035 1040
 Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser
 1045 1050 1055
 Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met
 1060 1065 1070
 Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe
 1075 1080 1085
 Leu *
 1090

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 187..3507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTTCTCCTG AGCCTTCAGG AGCCTGCACC AGTCCTGCCT GTCCTTCTAC TCAGCTGTTA	60
CCCACTCTGG GACCAGCAGT CTTTCTGATA ACTGGGAGAG GGCAGTAAGG AGGACTTCCT	120
GGAGGGGGTG ACTGTCCAGA GCCTGGAACG GTGCCACAC CAGAAGCCAT CAGCAGCAAG	180
GACACC ATG CGG CTT CCG GGT GCG ATG CCA GCT CTG GCC CTC AAA GGC	228
Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly	
1095 1100	
GAG CTG CTG TTG CTG TCT CTC CTG TTA CTT CTG GAA CCA CAG ATC TCT	276
Glu Leu Leu Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser	
1105 1110 1115 1120	
CAG GGC CTG GTC GTC ACA CCC CCG GGG CCA GAG CTT GTC CTC AAT GTC	324
Gln Gly Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val	
1125 1130 1135	
TCC AGC ACC TTC CTG ACC TGC TCG GGT TCA GCT CCG GTG GTG TGG	372
Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp	
1140 1145 1150	
GAA CGG ATG TCC CAG GAG CCC CCA CAG GAA ATG GCC AAG GCC CAG GAT	420
Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp	
1155 1160 1165	
GGC ACC TTC TCC AGC GTG CTC ACA CTG ACC AAC CTC ACT GGG CTA GAC	468
Gly Thr Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp	
1170 1175 1180	
ACG GGA GAA TAC TTT TGC ACC CAC AAT GAC TCC CGT GGA CTG GAG ACC	516
Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr	
1185 1190 1195 1200	
GAT GAG CGG AAA CGG CTC TAC ATC TTT GTG CCA GAT CCC ACC GTG GGC	564
Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly	
1205 1210 1215	
TTC CTC CCT AAT GAT GCC GAG GAA CTA TTC ATC TTT CTC ACG GAA ATA	612
Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile	
1220 1225 1230	
ACT GAG ATC ACC ATT CCA TGC CGA GTA ACA GAC CCA CAG CTG GTG GTG	660
Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val	
1235 1240 1245	
ACA CTG CAC GAG AAG AAA GGG GAC GTT GCA CTG CCT GTC CCC TAT GAT	708
Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp	
1250 1255 1260	
CAC CAA CGT GGC TTT TCT GGT ATC TTT GAG GAC AGA AGC TAC ATC TGC	756
His Gln Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys	
1265 1270 1275 1280	
AAA ACC ACC ATT GGG GAC AGG GAG GTG GAT TCT GAT GCC TAC TAT GTC	804
Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val	
1285 1290 1295	

TAC AGA CTC CAG GTG TCA TCC ATC AAC GTC TCT GTG AAC GCA GTG CAG	852
Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln	
1300 1305 1310	
ACT GTG GTC CGC CAG GGT GAG AAC ATC ACC CTC ATG TGC ATT GTG ATC	900
Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile	
1315 1320 1325	
GGG AAT GAT GTG GTC AAC TTC GAG TGG ACA TAC CCC CGC AAA GAA AGT	948
Gly Asn Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser	
1330 1335 1340	
GGG CGG CTG GTG GAG CCG GTG ACT GAC TTC CTC TTG GAT ATG CCT TAC	996
Gly Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr	
1345 1350 1355 1360	
CAC ATC CGC TCC ATC CTG CAC ATC CCC AGT GCC GAG TTA GAA GAC TCG	1044
His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser	
1365 1370 1375	
GGG ACC TAC ACC TGC AAT GTG ACG GAG AGT GTG AAT GAC CAT CAG GAT	1092
Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp	
1380 1385 1390	
GAA AAG GCC ATC AAC ATC ACC GTG GTT GAG AGC GGC TAC GTG CGG CTC	1140
Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu	
1395 1400 1405	
CTG GGA GAG GTG GGC ACA CTA CAA TTT GCT GAG CTG CAT CGG AGC CGG	1188
Leu Gly Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg	
1410 1415 1420	
ACA CTG CAG GTA GTG TTC GAG GCC TAC CCA CCG CCC ACT GTC CTG TGG	1236
Thr Leu Gln Val Val Phe Glu Ala Tyr Pro Pro Thr Val Leu Trp	
1425 1430 1435 1440	
TTC AAA GAC AAC CGC ACC CTG GGC GAC TCC AGC GCT GGC GAA ATC GCC	1284
Phe Lys Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala	
1445 1450 1455	
CTG TCC ACG CGC AAC GTG TCG GAG ACC CGG TAT GTG TCA GAG CTG ACA	1332
Leu Ser Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr	
1460 1465 1470	
CTG GTT CGC GTG AAG GTG GCA GAG GCT GGC CAC TAC ACC ATG CGG GCC	1380
Leu Val Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala	
1475 1480 1485	
TTC CAT GAG GAT GCT GAG GTC CAG CTC TCC TTC CAG CTA CAG ATC AAT	1428
Phe His Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn	
1490 1495 1500	
GTC CCT GTC CGA GTG CTG GAG CTA AGT GAG AGC CAC CCT GAC AGT GGG	1476
Val Pro Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly	
1505 1510 1515 1520	
GAA CAG ACA GTC CGC TGT CGT GGC CGG GGC ATG CCG CAG CCG AAC ATC	1524
Glu Gln Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile	
1525 1530 1535	
ATC TGG TCT GCC TGC AGA GAC CTC AAA AGG TGT CCA CGT GAG CTG CCG	1572
Ile Trp Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro	
1540 1545 1550	
CCC ACG CTG CTG GGG AAC AGT TCC GAA GAG GAG AGC CAG CTG GAG ACT	1620
Pro Thr Leu Leu Gly Asn Ser Ser Glu Glu Ser Gln Leu Glu Thr	
1555 1560 1565	

AAC GTG ACG TAC TGG GAG GAG GAG CAG GAG TTT GAG GTG GTG AGC ACA	1668
Asn Val Thr Tyr Trp Glu Glu Glu Gln Glu Phe Glu Val Val Ser Thr	
1570 1575 1580	
CTG CGT CTG CAG CAC GTG GAT CGG CCA CTG TCG GTG CGC TGC ACG CTG	1716
Leu Arg Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu	
1585 1590 1595 1600	
CGC AAC GCT GTG GGC CAG GAC ACG CAG GAG GTC ATC GTG GTG CCA CAC	1764
Arg Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His	
1605 1610 1615	
TCC TTG CCC TTT AAG GTG GTG ATC TCA GCC ATC CTG GCC CTG GTG	1812
Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val	
1620 1625 1630	
GTG CTC ACC ATC ATC TCC CTT ATC ATC CTC ATC ATG CTT TGG CAG AAG	1860
Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys	
1635 1640 1645	
AAG CCA CGT TAC GAG ATC CGA TGG AAG GTG ATT GAG TCT GTG AGC TCT	1908
Lys Pro Arg Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser	
1650 1655 1660	
GAC GGC CAT GAG TAC ATC TAC GTG GAC CCC ATG CAG CTG CCC TAT GAC	1956
Asp Gly His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp	
1665 1670 1675 1680	
TCC ACG TGG GAG CTG CCG CGG GAC CAG CTT GTG CTG GGA CGC ACC CTC	2004
Ser Thr Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu	
1685 1690 1695	
GGC TCT GGG GCC TTT GGG CAG GTG GTG GAG GCC ACA GCT CAT GGT CTG	2052
Gly Ser Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu	
1700 1705 1710	
AGC CAT TCT CAG GCC ACG ATG AAA GTG GCC GTC AAG ATG CTT AAA TCC	2100
Ser His Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser	
1715 1720 1725	
ACA GCC CGC AGC AGT GAG AAG CAA GCC CTT ATG TCG GAG CTG AAG ATC	2148
Thr Ala Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile	
1730 1735 1740	
ATG AGT CAC CTT GGG CCC CAC CTG AAC GTG GTC AAC CTG TTG GGG GCC	2196
Met Ser His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala	
1745 1750 1755 1760	
TGC ACC AAA GGA GGA CCC ATC TAT ATC ATC ACT GAG TAC TGC CGC TAC	2244
Cys Thr Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr	
1765 1770 1775	
GGA GAC CTG GTG GAC TAC CTG CAC CGC AAC AAA CAC ACC TTC CTG CAG	2292
Gly Asp Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln	
1780 1785 1790	
CAC CAC TCC GAC AAG CGC CGC CCG CCC AGC GCG GAG CTC TAC AGC AAT	2340
His His Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn	
1795 1800 1805	
GCT CTG CCC GTT GGG CTC CCC CTG CCC AGC CAT GTG TCC TTG ACC GGG	2388
Ala Leu Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly	
1810 1815 1820	
GAG AGC GAC GGT GGC TAC ATG GAC ATG AGC AAG GAC GAG TCG GTG GAC	2436
Glu Ser Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp	
1825 1830 1835 1840	

TAT GTG CCC ATG CTG GAC ATG AAA GGA GAC GTC AAA TAT GCA GAC ATC Tyr Val Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile 1845 1850 1855	2484
GAG TCC TCC AAC TAC ATG GCC CCT TAC GAT AAC TAC GTT CCC TCT GCC Glu Ser Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala 1860 1865 1870	2532
CCT GAG AGG ACC TGC CGA GCA ACT TTG ATC AAC GAG TCT CCA GTG CTA Pro Glu Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu 1875 1880 1885	2580
AGC TAC ATG GAC CTC GTG GGC TTC AGC TAC CAG GTG GCC AAT GGC ATG Ser Tyr Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met 1890 1895 1900	2628
GAG TTT CTG GCC TCC AAG AAC TGC GTC CAC AGA GAC CTG GCG GCT AGG Glu Phe Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg 1905 1910 1915 1920	2676
AAC GTG CTC ATC TGT GAA GGC AAG CTG GTC AAG ATC TGT GAC TTT GGC Asn Val Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly 1925 1930 1935	2724
CTG GCT CGA GAC ATC ATG CGG GAC TCG AAT TAC ATC TCC AAA GGC AGC Leu Ala Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser 1940 1945 1950	2772
ACC TTT TTG CCT TTA AAG TGG ATG GCT CCG GAG AGC ATC TTC AAC AGC Thr Phe Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser 1955 1960 1965	2820
CTC TAC ACC ACC CTG AGC GAC GTG TGG TCC TTC GGG ATC CTG CTC TGG Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp 1970 1975 1980	2868
GAG ATC TTC ACC TTG GGT GGC ACC CCT TAC CCA GAG CTG CCC ATG AAC Glu Ile Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn 1985 1990 1995 2000	2916
GAG CAG TTC TAC AAT GCC ATC AAA CGG GGT TAC CGC ATG GCC CAG CCT Glu Gln Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro 2005 2010 2015	2964
GCC CAT GCC TCC GAC GAG ATC TAT GAG ATC ATG CAG AAG TGC TGG GAA Ala His Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu 2020 2025 2030	3012
GAG AAG TTT GAG ATT CGG CCC CCC TTC TCC CAG CTG GTG CTG CTT CTC Glu Lys Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu 2035 2040 2045	3060
GAG AGA CTG TTG GGC GAA GGT TAC AAA AAG AAG TAC CAG CAG GTG GAT Glu Arg Leu Leu Gly Glu Gly Tyr Lys Lys Tyr Tyr Gln Gln Val Asp 2050 2055 2060	3108
GAG GAG TTT CTG AGG AGT GAC CAC CCA GCC ATC CTT CGG TCC CAG GCC Glu Glu Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala 2065 2070 2075 2080	3156
CGC TTG CCT GGG TTC CAT GGC CTC CGA TCT CCC CTG GAC ACC AGC TCC Arg Leu Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser 2085 2090 2095	3204
GTC CTC TAT ACT GCC GTG CAG CCC AAT GAG GGT GAC AAC GAC TAT ATC Val Leu Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile 2100 2105 2110	3252

ATC CCC CTG CCT GAC CCC AAA CCT GAG GTT GCT GAC GAG GGC CCA CTG Ile Pro Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu 2115 2120 2125	3300
GAG GGT TCC CCC AGC CTA GCC AGC TCC ACC CTG AAT GAA GTC AAC ACC Glu Gly Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr 2130 2135 2140	3348
TCC TCA ACC ATC TCC TGT GAC AGC CCC CTG GAG CCC CAG GAC GAA CCA Ser Ser Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro 2145 2150 2155 2160	3396
GAG CCA GAG CCC CAG CTT GAG CTC CAG GTG GAG CCG GAG CCG GAG CTG Glu Pro Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu 2165 2170 2175	3444
GAA CAG TTG CCG GAT TCG GGG TGC CCT GCG CCT CCG GCG GAA GCA GAG Glu Gln Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu 2180 2185 2190	3492
GAT AGC TTC CTG TAG GGGGCTGGCC CCTACCTGC CCTGCCTGAA GCTCCCCCGC Asp Ser Phe Leu * 2195	3547
TGCCAGCACC CAGCATCTCC TGGCCTGGCC TGGCCGGGCT TCCTGTCAGC CAGGCTGCC TTATCAGCTG TCCCCTCTG GAAGCTTCT GCTCCTGACG TGTGTGCC CAAACCTGG GGCTGGCTTA GGAGGCAAGA AAAC TGCAAGG GGCGTGACCC AGCCCTCTGC CTCCAGGGAG GCCAACTGAC TCTGAGCCAG GGTTCCCCCA GGGAACTCAG TTTTCCCATA TGTAAGATGG GAAAGTTAGG CTTGATGACC CAGAATCTAG GATTCTCTCC CTGGCTGACA GGTGGGGAGA CCGAATCCCT CCCTGGGAAG ATTCTTGAG TTACTGAGGT GGTAAATTAA CTTTTTCTG TTCAGCCAGC TACCCCTCAA GGAATCATAG CTCTCTCCTC GCACTTTAT CCACCCAGGA GCTAGGGAAAG AGACCTAGC CTCCCTGGCT GCTGGCTGAG CTAGGGCTA GCCTTGAGCA GTGTTGCCCTC ATCCAGAAGA AAGCCAGTCT CCTCCCTATG ATGCCAGTCC CTGCGTTCCC TGGCCCGAGC TGGCTGGGG CCATTAGGCA GCCTAATTAA TGCTGGAGGC TGAGCCAAGT ACAGGACACC CCCAGCCTGC AGCCCTTGCC CAGGGCACTT GGAGCACACG CAGCCATAGC AAGTGCCTGT GTCCCTGTCC TTCAGGCCA TCAGTCCTGG GGCTTTTCT TTATCACCC CAGTCTTAAT CCATCCACCA GAGTCTAGAA GGCCAGACGG GCCCCGCATC TGTGATGAGA ATGTAAATGT GCCAGTGTGG AGTGGCCACG TGTGTGTGCC AGATATGGCC CTGGCTCTGC ATTGGACCTG CTATGAGGCT TTGGAGGAAT CCCTCACCCCT CTCTGGGCCT CAGTTCCCC TTCAAAAAAT GAATAAGTCG GACTTATTAA CTCTGAGTGC CTTGCCAGCA CTAACATTCT AGAGTATCCA GGTGGTTGCA CATTGTCGA GATGAAGCAA GGCCATATAC CCTAAACTTC CATCCTGGGG GTCAGCTGGG CTCCCTGGAG ATTCCAGATC ACACATCACA CTCTGGGAC TCAGGAACCA TGCCCTTCC CCAGGCCCCC AGCAAGTCTC AAGAACACAG CTGCACAGGC CTTGACTTAG AGTGACAGCC GGTGTCTGG AAAGCCCCA GCAGCTGCC CAGGGACATG GGAAGACCAC GGGACCTCTT TCACTACCCA CGATGACCTC CGGGGGTATC CTGGGCAAAA GGGACAAAGA GGGCAAATGA GATCACCTCC TGCAGCCAC CACTCCAGCA CCTGTGCCGA	3607 3667 3727 3787 3847 3907 3967 4027 4087 4147 4207 4267 4327 4387 4447 4507 4567 4627 4687 4747 4807 4867

GGTCTGCGTC GAAGACAGAA TGGACAGTGA GGACAGTTAT GTCTTGTAAA AGACAAGAAG	4927
CTTCAGATGG GTACCCCAAG AAGGATGTGA GAGGTGGCG CTTTGGAGGT TTGCCCCCTCA	4987
CCCACCAGCT GCCCCATCCC TGAGGCAGCG CTCCATGGGG GTATGGTTTT GTCACTGCC	5047
AGACCTAGCA GTGACATCTC ATTGTCCCCA GCCCAGTGGG CATTGGAGGT GCCAGGGGAG	5107
TCAGGGTTGT AGCCAAGACG CCCCCGCACG GGGAGGGTTG GGAAGGGGT GCAGGAAGCT	5167
CAACCCCTCT GGGCACCAAC CCTGCATTGC AGGTTGGCAC CTTACTTCCC TGGGATCCCA	5227
GAGTTGGTCC AAGGAGGGAG AGTGGGTCT CAATACGGTA CCAAAGATAT AATCACCTAG	5287
GTTTACAAAT ATTTTAGGA CTCACGTTAA CTCACATTAA TACAGCAGAA ATGCTATTTT	5347
GTATGCTGTT AAGTTTTCT ATCTGTGTAC TTTTTTTAA GGGAAAGATT TTAATATTA	5407
ACCTGGTGCT TCTCACTCAC	5427

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu	
1 5 10 15	
Leu Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly	
20 25 30	
Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser	
35 40 45	
Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg	
50 55 60	
Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr	
65 70 75 80	
Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly	
85 90 95	
Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu	
100 105 110	
Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu	
115 120 125	
Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu	
130 135 140	
Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu	
145 150 155 160	
His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln	
165 170 175	
Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr	
180 185 190	

Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg
 195 200 205

Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val
 210 215 220

Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn
 225 230 235 240

Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg
 245 250 255

Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile
 260 265 270

Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr
 275 280 285

Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys
 290 295 300

Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly
 305 310 315 320

Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu
 325 330 335

Gln Val Val Phe Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp Phe Lys
 340 345 350

Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser
 355 360 365

Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr Leu Val
 370 375 380

Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala Phe His
 385 390 395 400

Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn Val Pro
 405 410 415

Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly Glu Gln
 420 425 430

Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile Ile Trp
 435 440 445

Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro Pro Thr
 450 455 460

Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr Asn Val
 465 470 475 480

Thr Tyr Trp Glu Glu Glu Gln Glu Phe Glu Val Val Ser Thr Leu Arg
 485 490 495

Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu Arg Asn
 500 505 510

Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
 515 520 525

Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
 530 535 540

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
 545 550 555 560
 Arg Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly
 565 570 575
 His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr
 580 585 590
 Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser
 595 600 605
 Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His
 610 615 620
 Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala
 625 630 635 640
 Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile Met Ser
 645 650 655
 His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr
 660 665 670
 Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp
 675 680 685
 Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln His His
 690 695 700
 Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu
 705 710 715 720
 Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly Glu Ser
 725 730 735
 Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val
 740 745 750
 Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile Glu Ser
 755 760 765
 Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala Pro Glu
 770 775 780
 Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser Tyr
 785 790 795 800
 Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe
 805 810 815
 Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val
 820 825 830
 Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala
 835 840 845
 Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe
 850 855 860
 Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr
 865 870 875 880
 Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile
 885 890 895

Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu L u Pro Met Asn Glu Gln
 900 905 910

Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His
 915 920 925

Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys
 930 935 940

Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Glu Arg
 945 950 955 960

Leu Leu Gly Glu Gly Tyr Lys Lys Tyr Gln Gln Val Asp Glu Glu
 965 970 975

Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu
 980 985 990

Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu
 995 1000 1005

Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile Pro
 1010 1015 1020

Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu Glu Gly
 1025 1030 1035 1040

Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser
 1045 1050 1055

Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu Pro
 1060 1065 1070

Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln
 1075 1080 1085

Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser
 1090 1095 1100

Phe Leu *
 1105

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
 1 5 10 15

Met Leu Asp Met
 20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719P. Contains a phosphate group at position 14."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
1 5 10 15

Met Leu Asp Met
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708P. Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
1 5 10 15

Met Leu Asp Met
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Peptide Y719P short."

Contains a phosphate group at position 11."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro Met Leu Asp
 1 5 10 15

Met

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "Peptide Y708P short.

Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp
 1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708P/F719.

Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Phe Val Pro
 1 5 10 15

Met Leu Asp Met
 20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708/Y719P.

Contains a phosphate group at position 14."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly	Gly	Phe	Met	Asp	Met	Ser	Lys	Asp	Glu	Ser	Ile	Asp	Tyr	Val	Pro
1				5					10					15	
Met	Leu	Asp	Met												
			20												

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708P/Y719P.

Contains phosphate group at positions 3 & 14"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly	Gly	Tyr	Met	Asp	Met	Ser	Lys	Asp	Glu	Ser	Ile	Asp	Tyr	Val	Pro
1				5					10					15	
Met	Leu	Asp	Met												
			20												

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719P scrambled.

Contains a phosphate group at position 15."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Met	Asp	Ile	Lys	Val	Pro	Met	Asp	Glu	Tyr	Met	Ser	Asp	Tyr	Ser
1				5					10					15	

Asp Leu Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURES:

- (D) OTHER INFORMATION: /note= "N is A, C, G, or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTSCGNGCN GCCAGNTCSC GNTG

24